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ADRB2 Haplotypes and Asthma Exacerbations in Children and Young Adults: An Individual Participant Data Meta-Analysis

Running Title: *ADRB2* Haplotypes and Asthma Exacerbations

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Graphical Abstract Text

Asthmatic children and young adults treated with inhaled corticosteroid (ICS) plus long-acting β_2-agonists (LABA) were more prone to asthma exacerbations if they were carriers of *ADRB2* haplotype (Arg16Gln27) compared to non-carriers. The *ADRB2* Arg16 haplotype, presumably mainly driven by the Arg16, increased the risk of asthma exacerbations in patients treated with ICS plus LABA. This finding could be beneficial in *ADRB2* genotype-guided asthma treatment and might improve patient outcomes.

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KEY MESSAGE:

- Response to treatment with inhaled corticosteroids (ICS) and long-acting β_2-agonists (LABA) varies inter-individually in asthmatic patients.
- The *ADRB2* Arg16 haplotype increased the risk of asthma exacerbations in patients treated with ICS plus LABA.
- This finding could be beneficial in *ADRB2* genotype-guided treatment in asthmatic patients.

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ABSTRACT

Background: The polymorphism Arg16 in β_2-adrenergic receptor (*ADRB2*) gene has been associated with an increased risk of exacerbations in asthmatic children treated with long-acting β_2-agonists (LABA). However, it remains unclear whether this increased risk is mainly attributed to this single variant or the combined effect of the haplotypes of polymorphisms at codons 16 and 27.

Objective: We assessed whether the haplotype analysis could explain the association between the polymorphisms at codons 16 (Arg16Gly) and 27 (Gln27Glu) in *ADRB2* and risk of asthma exacerbations in patients treated with inhaled corticosteroids (ICS) plus LABA.

Methods: The study was undertaken using data from ten independent studies (n = 5,903) of the multi-ethnic Pharmacogenomics in Childhood Asthma (PiCA) consortium. Asthma exacerbations were defined as asthma-related use of oral corticosteroids or hospitalizations/emergency department visits in the past 6 or 12 months prior to the study visit/enrolment. The association between the haplotypes and the risk of asthma exacerbations was performed per study using haplo.stats package adjusted for age and sex. Results were meta-analyzed using the inverse variance weighting method assuming random-effects.

Results: In subjects treated with ICS and LABA (n = 832, age: 3-21 years), Arg16/Gln27 vs. Gly16/Glu27 (OR: 1.40, 95% CI: 1.05-1.87, $I^2 = 0.0\%$) and Arg16/Gln27 vs. Gly16/Gln27 (OR: 1.43, 95% CI: 1.05-1.94, $I^2 = 0.0\%$), but not Gly16/Gln27 vs. Gly16/Glu27 (OR: 0.99, 95% CI: 0.71-1.39, $I^2 = 0.0\%$), were significantly associated with an increased risk of asthma exacerbations. The sensitivity analyses indicated no significant association between the *ADRB2* haplotypes and asthma exacerbations in the other treatment categories i.e., as-required short-acting β_2-agonists (n = 973), ICS monotherapy (n = 2,623), ICS plus leukotriene receptor antagonists (LTRA; n = 338), or ICS plus LABA plus LTRA (n = 686).

Conclusion and clinical relevance: The *ADRB2* Arg16 haplotype, presumably mainly driven by the Arg16, increased the risk of asthma exacerbations in patients treated with ICS plus LABA. This finding could be beneficial in *ADRB2* genotype-guided treatment which might improve clinical outcomes in asthmatic patients.

Keywords: asthma exacerbations; long-acting β_2-agonists; inhaled corticosteroids; *ADRB2*; haplotypes

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INTRODUCTION

Asthma is a common, heterogeneous, and chronic respiratory disease. Despite treatment, patients might experience exacerbations that can be life-threating. The combination therapy of inhaled corticosteroids (ICS) and long-acting β_2-agonists (LABA) is one of the recommended treatments for the control of asthma in children.[1] However, response to treatment with LABA varies inter-individually and this might be partly mediated by genetic variation.[2]

The β_2-adrenergic receptor is a member of the G protein-coupled transmembrane receptors broadly located on airway smooth muscle cells.[3] The β_2-adrenergic receptor (*ADRB2*) gene, a small intron-less gene on chromosome 5q31.32, encodes the receptor and contains different single nucleotide polymorphisms (SNPs). Of these SNPs, the coding non-synonymous variants rs1042713 (Arg16Gly), a Glycine-to-Arginine amino acid substitution at codon 16, and rs1042714 (Gln27Glu), a Glutamine-to-Glutamic acid amino acid substitution at codon 27, that are in linkage disequilibrium, have been found to be associated with asthma and asthma phenotypes.[4-6]

Although various studies have investigated the association between the *ADRB2* polymorphisms and response to LABA, the results are conflicting and inconclusive.[7-11] A recent meta-analysis in the Pharmacogenomics in Childhood Asthma[12] (PiCA) consortium showed that asthmatic children carrying 1 or 2 Arg allele(s) at rs1042713 and treated with ICS plus LABA have an increased risk of exacerbations.[10] Previous studies showed that the Gln allele at rs1042714 was a risk factor for asthma and associated with a less effective response to treatment with inhaled β_2-agonists during an acute asthma exacerbation.[6,13] Furthermore, most studies, as well as the recent meta-analysis in the PiCA consortium,[10] evaluated the effect of each variant independently but not the combined effect of their haplotypes that might yield additional insight into the association between the *ADRB2* variants and asthma exacerbations. Therefore, it is still unclear whether the combined effect of the *ADRB2* polymorphisms at codons 16 and 27 is associated with an increased risk of asthma exacerbations or whether the association is driven by just the single polymorphism at codon 16.

Therefore, we aimed to assess whether the haplotype analysis could explain the association between the polymorphisms at codons 16 and 27 of *ADRB2* and the risk of asthma exacerbations in patients treated with ICS plus LABA.

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METHODS

Study population

Data from ten independent studies participating in the PiCA consortium[12] were analyzed. BREATHE is an observational study that includes children and young adults (age: 3-22 years)[14] with physician-diagnosed asthma recruited from primary and secondary care units in Tayside, Scotland, and Brighton, United Kingdom. The Effectiveness and Safety of Treatment with Asthma Therapy in children (ESTATe) is a case-control study that includes children and young adults (4-19 years) with physician-diagnosed asthma recruited from primary care units in the Netherlands. The followMAGICS study is the follow-up study of the observational Multicenter Asthma Genetics in Childhood Study (MAGICS), which includes physician-diagnosed asthmatic children and young adults (age: 7-25 years)[15] recruited from secondary and tertiary centers in Germany and Austria. The Genes-Environment and Admixture in Latino Americans (GALA II) and the Study of African Americans, Asthma, Genes, and Environments (SAGE) studies are two independent case-control asthma cohorts (age: 8-21 years) that focus on two different racial/ethnic groups based on the self-identified ethnicity of the four grandparents of each subject: Hispanics/Latinos (GALA II) and African Americans (SAGE) in the United States and Puerto Rico.[16,17] The Pharmacogenetics of Asthma Medication in Children: Medication with Anti-inflammatory effects (PACMAN) study in the Netherlands,[18] is an observational cohort study that included children (age: 4-12 years) with self-reported regular use of asthma medication recruited through community pharmacies. Children were selected from community pharmacies in the Netherlands that belonged to the Utrecht Pharmacy Practice Network for Education and Research (UPPER).[19] The Pediatric Asthma Gene Environment Study (PAGES) is a cross sectional observational study designed to relate asthma outcomes to environmental and genetic factors. Children (age: 5-16 years) with physician-diagnosed asthma were recruited from primary and secondary care centers across Scotland.[20] The Pharmacogenetics of Adrenal Suppression Study (PASS) in the United Kingdom (age: 5-18 years) is a multicenter cohort of asthmatic children. The study initially aimed to explore the association between use of corticosteroids and adrenal suppression, and how genetic factors influence this association.[21,22] The Singapore Cross Sectional Genetic Epidemiology Study (SCSGES)[23] (age: 6-31 years) is an ongoing cross-sectional genetic epidemiology study on allergic diseases among Singapore Chinese individuals. The ethnicity of subjects was self-reported Chinese and confirmed by principal component analysis. Asthma was defined by having a physician-diagnosis of symptoms prior to recruitment.[23,24] The SLOVENIA study is a case-control cohort (age: 5-18) and

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includes asthmatic children and young adults recruited from tertiary health centers from Murska Sobota, Slovenia.[25] Further details on the study population are described in the Supporting Information.

All studies have been approved by their local medical ethics committees/institutional review boards and parents or participants provided written consent. The Tayside Committee on Medical Research Ethics (Dundee, United Kingdom) approved BREATHE (reference number: NFB/FB/106/03). ESTATe was approved by the Medische Ethische Toetsings Commissie, Erasmus Medical Center (Rotterdam, the Netherlands) (reference number: MEC-2011-474). GALA II and SAGE were approved by the Human Research Protection Program Institutional Review Board of the University of California, San Francisco (San Francisco, United States) (reference numbers: 10-00889 and 10-02877 , respectively). PACMAN was approved by the Medical Ethics Committee of the University Medical Centre Utrecht (Utrecht, the Netherlands reference number: NL2124.021.08). PAGES has been approved by the Cornwall and Plymouth Research Ethics Committee (reference number: 07/H0203/204). PASS was approved by the Liverpool Pediatric Research Ethics Committee (Liverpool, United Kingdom, reference number: 08/H1002/56). SLOVENIA was approved by the Slovenian National Medical Ethics Committee (Ljubljana, Slovenia, reference number: 0120-569/2017/4). The Ethik- Kommission der Bayerischen Landesärztekammer (Munich, Germany) (reference number: 01218) and ethics committee of the medical University of Hannover (reference number: 1021-2011) approved followMAGICS. The ethical approval for the SCSGES cohort was obtained from the Institutional Review Board of the National University of Singapore (NUS-IRB), reference numbers: 07–023, 09–256, 10-343, 10–445 and 13–075 for the large scale epidemiology and genetics study and the Institutional Review Board of the National Healthcare Group Domain, Specific Review Board - B/04/055.

Medication data

Data on asthma treatment was collected either from pharmacy records, parent/patient-reported medication use, or completed study questionnaires (PACMAN, followMAGICS, BREATHE, GALA II, PAGES, SAGE, and SCSGES) or physician prescriptions and pharmacy records (ESTATe, PASS, and SLOVENIA). Asthma treatment was categorized as follows: (1) as-required short-acting β_2-agonists (SABA) (2) inhaled corticosteroids (ICS) monotherapy, (3) ICS in combination with LABA, (4) ICS in combination with leukotriene receptor antagonists (LTRA),

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and (5) ICS in combination with LABA and LTRA. All children in categories 2-5 used as-required SABA.

Main outcome

Asthma exacerbations, the main outcome, were defined based on the American Thoracic Society (ATS)/European Respiratory Society (ERS) guidelines as episodes of worsening of asthma symptoms which require a short course (3-5 days) of oral systemic corticosteroids (OCS) use, hospitalizations or emergency department (ED) visits.[26] Cases were determined if subjects had at least one asthma exacerbation (described above) in the past 6 or 12 months prior to the study visit or enrolment.

Data on asthma exacerbations, asthma-related OCS use or hospitalizations/ED visits, were reported by the parent/child at the study visit or based on study questionnaires or physician records: 1) BREATHE, and PASS: hospitalizations or OCS use in the past six months preceding the study visit; 2) PACMAN: ED visits or OCS use in the past 12 months preceding the study visit; 3) GALA II, SLOVENIA, ESTATe, SAGE, PAGES, and SCSGES: hospitalizations/ED visits or OCS use in the past 12 months preceding the study visit. In followMAGICS, only data on asthma-related hospitalizations or ED visits were available in the past 12 months preceding the study visit.[12]

Genotyping

In BREATH and PAGES, genotypes were determined by using Taqman-based allelic discrimination assays on an ABI 7,700 sequence detection system (Applied Biosystems, Foster City, Calif)[4,27] In followMAGICS, samples were genotyped using Illumina Sentrix HumanHap300 BeadChip array (Illumina, Inc.)[15] In both GALA II and SAGE, samples were genotyped using the Axiom® LAT1 array (Affymetrix Inc.), and quality control (QC) procedures were performed as described previously.[28,29] In PACMAN and ESTATe, samples were genotyped using the Illumina Infinium CoreExome-24 BeadChip (Illumina, Inc.).[30] In PASS, genotyping was performed using the Illumina Omni Express 8v1 array (Illumina, Inc.). QC procedures and imputation are described elsewhere.[22] In SCSGES, genotyping was conducted using Kompetitive Allele Specific PCR (KASP) genotyping platform (LGC, Inc). QC was performed based on the quality of clustering.[23] In the SLOVENIA study, genotyping of 336 samples was performed with the Illumina Global

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Screening Array-24 v1.0 BeadChip (Illumina). QC procedures and imputation described elsewhere.[30]

Functional annotation of variants and expression quantitative trait loci (eQTL) analysis

We used HaploRegv4.1 (http://www.broadinstitute.org/mammals/haploreg/haploreg.php)[31] to retrieve all proxy SNPs in strong linkage disequilibrium (LD) (r^2 threshold > 0.8, limit distance 100 kb, and population panel CEU using 1000 Genomes project) with rs1042713 and rs1042714 in *ADRB2* and to assess the predicted functions of the variants including protein structure, effects on gene regulation, and splicing. We also checked the correlation of the SNPs and their proxies with the expression level of *ADRB2* in whole blood using expression quantitative trait loci (eQTL) data from Genenetwork.[32]

Statistical analyses

Descriptive statistics were used to calculate means and standard deviations for continuous variables and percentages for categorical variables. Hardy-Weinberg equilibrium (HWE) was assessed for each SNP using a web program (http://www.oege.org/software/hwe-mr-calc.shtml) which uses the Pearson chi-squared test for HWE testing.[33] In our main analysis, we analyzed the association between haplotype combinations of polymorphisms at codons 16 and 27 of the *ADRB2* gene and asthma exacerbations in the category of children treated with ICS plus LABA. We used the haplo.stats package (version 1.7.7)[34] in R adjusting for age and sex in each study separately, and the resulting odds ratios (ORs) were meta-analyzed. The statistical methods of the haplo.stats package assume that all subjects are unrelated and linkage phase of the genetic markers is unknown.[34] To address potential heterogeneity between studies, we used the inverse variance weighting method assuming random-effects. We also reported I^2 and Cochran's Q-test of the meta-analysis.[35] Forest plots were made using the 'metafor' package in R (version 3.3.3).[36]

Data on asthma-related OCS use were not available in followMAGICS. Therefore, in a sensitivity analysis, we repeated the haplotype analysis (as described above) separately for asthma-related hospitalizations/ED visits outcome as well as for asthma-related OCS use outcome. Furthermore, to test the robustness of our result in the treatment category of ICS plus LABA, we repeated the haplotype analysis (as described above) in the other treatment categories as follows; as-required SABA, ICS monotherapy, ICS plus LTRA, and ICS plus LTRA plus LABA. Since we

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181 investigated the association of haplotype combinations of two polymorphisms and asthma
182 exacerbations, we considered a P-value less than 0.025 (0.05/2) for our main meta-analysis to be
183 statistically significant.

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RESULTS

Study characteristics

The characteristics of the study populations (for each study) are presented in Table 1. Data on age, sex, and treatment were available for 5,903 children and young adults. Out of these 5,903 subjects, data on asthma exacerbations were available in 5,726 subjects.

Asthma exacerbations occurred in 2,494 patients (43.5%) and the proportion of asthma exacerbations ranged from 9.7% (PACMAN) to 86.2% (PASS) across the studies. The mean age (SD) of the patients ranged between 8.7 (2.3) years for PACMAN and 17.3 (3.0) years for followMAGICS, and in all studies, the majority of patients were male. The percentage of subjects treated with ICS plus LABA differed across the studies and ranged from 10.2% in GALA II to 50.3% in followMAGICS. In addition, all patients in SLOVENIA and SCSGES were treated with ICS monotherapy.

Table 2 shows the *ADRB2* genotype and haplotype data. The risk allele (Arg) frequency for rs1042713 was highest in SCSGES, (0.55) followed by SAGE, (0.51). The risk allele (Arg) frequency for rs1072713 ranged between (0.34) for ESTATe and (0.41) for PACMAN across the European studies. The risk allele (Gln) frequency for rs1042714 was highest in SCSGES (0.93) followed by SAGE, (0.82). The risk allele (Gln) frequency for rs1042714 was similar across the European studies and ranged between (0.54) for PASS and (0.60) for ESTATe and SLOVENIA. Both SNPs were in HWE in all studies (in each cohort) and they showed a complete LD (D' ~ 1) with r^2 that ranged from 0.10 in SCSGES to 0.50 in PASS.

Three haplotypes were determined at positions 16 and 27, and haplotype frequencies were as follows: Arg16/Gln27 (ranged from 0.34 to 0.55), Gly16/Gln27 (ranged from 0.17 to 0.37), and Gly16/Glu27 (ranged from 0.08 to 0.46), (Table 2).

Risk of asthma exacerbations in children treated with ICS plus LABA

Data on the outcome, asthma exacerbations (asthma-related OCS use or hospitalizations/ED visits), haplotypes, and ICS plus LABA treatment were available in seven studies (n = 832 , age = 3-21 years). The meta-analysis indicated that Arg16/Gln27 vs. Gly16/Glu27 (OR: 1.40, 95% CI: 1.05-1.87, $I^2 = 0.00\%$, P = 0.022) and Arg16/Gln27 vs. Gly16/Gln27 (OR: 1.43, 95% CI: 1.05-1.94, $I^2 = 0.00\%$, P = 0.023), were significantly associated with an increased risk of asthma

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213 exacerbations (Figure 1). However, Gly16/Gln27 vs. Gly16/Glu27 (OR: 0.99, 95% CI: 0.71-1.39,
214 I^2 = 0.00%, P = 0.946), was not associated with the risk of asthma exacerbations.

215 **Sensitivity analyses**

216 In patients treated with ICS plus LABA, we repeated the haplotype analysis separately for asthma-
217 related OCS use and for asthma-related hospitalizations/ED visits. We observed the similar trends
218 as the main analysis (Figure 2 and Figure 3). Furthermore, no association between the *ADRB2*
219 haplotypes and the risk of asthma exacerbations was observed in any of the other treatment groups
220 (Table 3).

221 **Functional annotation and eQTL analysis of the *ADRB2* variants**

222 Functional annotation, using Haploreg v4.1 data,[31] showed that rs1042713 and rs1042714 had
223 several proxy variants in strong LD (D` = 1 and r^2 > 0.8), but none of them was a non-synonymous
224 proxy (Table S1 and Table S2 in the Supporting Information). Furthermore, the cis-eQTL data
225 from Genenetwork showed that not only the Arg allele of rs1042713 but also the Gln allele of
226 rs1042714 was associated with reduced levels expression of *ADRB2* in whole blood.[32] Therefore,
227 these data indicated that the variants alters the *ADRB2* expression and function.

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DISCUSSION

In this large multi-ethnic meta-analysis, we observed that the Arg16/Gln27 haplotype vs. the Gly16/Glu27 haplotype and the Arg16/Gln27 haplotype vs. the Gly16/Gln27 haplotype were associated with an increased risk of asthma exacerbations in children and young adults treated with ICS plus LABA. Considering that no statistically significant association was observed between the Gly16/Gln27 haplotype vs. the Gly16/Glu27 haplotype and the risk of asthma exacerbations, we could conclude that the combined effect of two polymorphisms at codons 16 and 27 on asthma exacerbations is presumably mainly driven by the Arg16. Furthermore, we did not find an increased risk for exacerbations in asthmatic children carrying the Arg16 haplotype in any of the other treatment categories. The lack of association in the treatment category containing ICS, LABA, and LTRA might be due to both the bronchodilation and anti-inflammation effects of LTRA[37], as well as to the relatively small sample size.

There was no heterogeneity ($I^2 = 0.00\%$) in the main analysis between studies (Figure 1); however, the ORs were slightly different across the studies. The proportion of asthma exacerbations largely varied between the studies, lowest in PACMAN (recruiting from primary care and community pharmacies) and highest in PASS (recruiting from tertiary care), which might be due to the recruitment of patients from different health care settings (i.e., primary, secondary, and tertiary care, or community pharmacies) and thus reflect differences in asthma severity. Also, asthma treatment policy that affects doctors' underlying tendencies to prescribe OCS varies in different countries, which in turn could influence the proportion of asthma exacerbations.[38] In all studies, both SNPs were in complete linkage disequilibrium (D`~1) with each other; as a result, we determined three haplotypes of the four possible haplotypes (Arg16/Glu27 was not reported), which is in line with previous findings.[39,40] Furthermore, considering ethnicity variability in our study populations, we observed different minor allele frequencies in each SNP that resulted in considerable variations in r^2, which indicates the correlation coefficient of the allele frequencies. We also observed the highest risk allele frequencies (the Arg allele at rs1042713 and the Gln allele at rs1042714) in SCSGES, SAGE, and GALA II, whereas the Gly16/Glu 27 haplotype frequency was substantially the lowest in these three studies, consistent with previous works.[41-46]

A recent systematic review[2] reported studies that investigated the association between the *ADRB2* variants and response to LABA in children and adults with asthma. In children, most studies reported an increased risk of asthma exacerbations in carriers of Arg 16, whereas no association

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was found in adults.[4,7,8,10,47] So far, only two studies investigated the effect of rs1042714 on asthma exacerbations in children treated with ICS plus LABA and did not report significant associations.[4,9] Similarly, in adults, no association between rs1042714 and response to LABA concerning asthma exacerbations has been shown in a post hoc analysis from a randomized clinical trial.[8]

A few studies examined the association between these *ADRB2* haplotypes in subjects with asthma. However, they mainly focused on changes in forced expiratory volume in 1 second (FEV_1),[42] forced vital capacity (FVC), FEV_1/FVC ratio,[43] and overall mean changes in morning peak flow as primary outcomes.[48] To the best of our knowledge, this is the first large meta-analysis investigating the association between the *ADRB2* haplotypes and the risk of asthma exacerbations in patients treated with ICS plus LABA to this date. We know from the literature that Arg16 at rs1042713 is associated with an increased risk for asthma exacerbations; however, this association has not yet been investigated in the Arg haplotype carriers.[4,5,10]

The exact mechanism by which *ADRB2* polymorphisms confer risk for asthma exacerbations in patients treated with ICS plus LABA is still unknown. The mechanism(s) underlying the association between the Arg16 allele and an increased risk of exacerbations in asthmatic patients treated with ICS plus LABA might involve an enhanced agonist-induced downregulation and uncoupling of airway β_2-receptor, resulting in subsensitivity of bronchoprotective response.[49] There is some evidence from the literature that *ADRB2* haplotypes regulate receptor transcript and protein expression.[42] Previous *in-vitro* findings indicated that the expression of the Arg16/Gln27 haplotype was significantly lower than the Gly16/Glu27 haplotype.[42] The latter results[42] are in line with eQTL data,[32] demonstrating decreased expression levels of *ADRB2* in the carriers of Arg16 and Gln27. Another possible explanation, based on the dynamic baseline receptor model proposed by Liggett,[50] could be that the Arg16 genotype would be slightly more resistant than the Gly16 genotype to endogenous downregulation and desensitization. Thus the Arg 16 genotype would remain more susceptible to further subsensitivity to the chronic use of exogenous agonists.[50] Hence, the observed weakened response to LABA in carriers of the Arg16/Gln27 haplotype is plausible.

As for all observational research, our study has strengths and limitations. The current study is to be the largest meta-analysis investigating the combined effect of the *ADRB2* variants in asthmatic

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patients treated with ICS plus LABA. Also, we used quality-controlled genotyping data, physician diagnosed-asthma, and relevant clinical outcomes (asthma exacerbations). As the first limitation, we did not determine haplotype frequency using gene-counting estimates based on phase-known data. Instead, we obtained haplotype frequency estimates using the expectation-maximization (E-M) algorithm that previous studies have demonstrated the usefulness of this approach (E-M method),[51] and the validity of the statistical technique of this method.[52] Second, although the *ADRB2* rare variants could affect treatment response to LABA therapy,[53] our study was not powered to conduct rare variant analysis. Third, as we lacked information on treatment adherence and dosing in some of the PiCA cohorts, we could not adjust for these factors in our analyses. Fourth, as gene expression and eQTL are tissue-specific, ideally, they should be examined in the lung tissue of patients with asthma, treated with ICS plus LABA. Finally, in our meta-analysis, we observed a significant OR (1.40), 95% CI (1.05-1.87) with a P = 0.022, applying a multiple testing correction (P < 0.025) to define statistically significant results. We also calculated a prediction interval (PI); the PI in a random-effects model contains a highly probable effect estimate (OR) for a future observation if a new setting is similar to those included in the meta-analysis.[54,55] In this case, the 95% PI is (0.96-2.04), and thus indeed broader than the 95% CI.

In conclusion, we found that the Arg16 haplotype in *ADRB2*, presumably mainly driven by the Arg16, increased the risk of asthma exacerbations among users of ICS and LABA. The clinical benefits and risks associated with the use of LABA in patients with the Arg16 haplotype and genotypes need to be evaluated in randomized clinical trials such as the ongoing precision medicine clinical trial (the PUFFIN trial) investigating *ADRB2* genotype-guided (the Arg16 genotype) treatment in children with asthma.[56]

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CONFLICT OF INTEREST

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Table 1: Characteristics of the study populations

Characteristics	BREATHE	ESTATe	Follow MAGICS	GALA II	PACMAN	PAGES	PASS	SAGE	SLOVENIA	SCSGES
n	998	101	167	1,618	791	722	384	740	212	170
Male sex, %	60.0	58.0	62.3	55.7	62.3	57.6	56.0	52.3	56.1	68.2
Mean age, y (SD)	10.2 (4.0)	10.6 (4.2)	17.3 (3.0)	12.4 (3.2)	8.7 (2.3)	9.8 (3.7)	11 (3.3)	13.8 (3.5)	10.8 (3.4)	14.0 (6.4)
Ethnicity, n. (%)										
Caucasian	998 (100)	96 (95)	167 (100)	N/A	711 (89.9)	360 (50)	384 (100)	N/A	212 (100)	N/A
Hispanic	N/A	N/A	N/A	1,618.(100)	3 (0.4)	N/A	N/A	744 (100)	N/A	N/A
Asian	N/A	1 (1)	N/A	N/A	6 (0.8)	11 (1.5)	N/A	N/A	N/A	170 (100)
African	N/A	0 (0)	N/A	N/A	9 (1.1)	N/A	N/A	N/A	N/A	N/A
Mixed	N/A	2 (2)	N/A	N/A	53 (6.7)	15 (2)	N/A	N/A	N/A	N/A
Unknown (missing)	N/A	2 (2)	N/A	N/A	9 (1.1)	336 (46.5)	N/A	N/A	N/A	N/A
Treatment group, n. (%)										
SABA alone	173 (17.3)	0 (0.0)	25 (15.0)	576 (35.6)	80 (10.1)	79 (10.9)	0 (0.0)	207 (27.9)	N/A	N/A
ICS alone	562 (56.3)	65 (64.0)	39 (23.3)	538 (33.2)	497 (62.8)	271 (37.6)	29 (7.5)	367 (49.6)	212 (100)	170 (100)
ICS + LABA	142 (14.3)	34 (34.0)	84 (50.3)	165 (10.2)	148 (18.7)	135 (18.7)	126 (33.0)	98 (13.2)	N/A	N/A
ICS + LTRA	37 (3.7)	0 (0.0)	4 (2.4)	208 (12.9)	21 (2.7)	65 (9.0)	0 (0.0)	35 (4.7)	N/A	N/A
ICS + LABA + LTRA	84 (8.4)	2 (2.0)	15 (9.0)	131 (8.1)	45 (5.7)	172 (23.8)	229 (59.5)	33 (4.6)	N/A	N/A
Asthma exacerbations in the past year or in the last six months prior to the study visit/enrolment										
Hospitalizations/ED*, n. (%)[#]	147 (14.7)	13 (12.9)	11 (6.6)	865 (54.8)	42 (5.5)	151 (21.7)	290 (75.5)	272 (39.0)	49 (27.7)	34 (20.0)
OCS use*, n. (%)[#]	234 (23.4)	36 (35.6)	N/A	587 (37.4)	46 (5.8)	316 (45.7)	198 (51.6)	162 (22.4)	23 (12.9)	36 (21.2)
Asthma exacerbations*, n. (%)[#]	250 (25.0)	49 (48.5)	N/A	1,013 (64.3)	75 (9.7)	346 (50.0)	331 (86.2)	317 (45.8)	54 (30.3)	59 (34.7)

N/A. Not Applicable; *ED, emergency department visits; OCS use, oral corticosteroids use; Asthma exacerbations, asthma-related hospitalizations/ED visits or oral corticosteroids use. [#]Data on asthma-related hospitalizations/ED visits outcomes were missing in 40 subjects in GALA II, 24 subjects in PACMAN, 27 subjects in PAGES, 43 subjects in SAGE, and 35 subjects in SLOVENIA; data on asthma-related oral OCS use were missing in 49 subjects in GALA II, 30 subjects in PAGES, 16 subjects in SAGE, and 34 subjects in

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SLOVENIA, data on asthma exacerbations were missing in 44 subjects in GALA II, 21 subjects in PACMAN, 30 subjects in PAGES, 48 subjects in SAGE, and 34 subjects in SLOVENIA. In followMAGICS, only data on asthma-related hospitalizations/ED visits were available.

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Table 2: *ADRB2* genotype and haplotype data

Characteristics	BREATHE	ESTATe	Follow MAGICS	GALAII	PACMAN	PAGES	PASS	SAGE	SLOVENIA	SCSGES
Subjects with data on rs1042713. n.	998	101	167	1,618	791	720	384	740	212	170
Risk allele (Arg) frequency	0.37	0.34	0.38	0.44	0.41	0.37	0.37	0.51	0.37	0.55
rs1042713 genotype, no. (%)										
Arg/Arg	154 (15.4)	14 (13.9)	25 (15.0)	306 (18.9)	124 (15.7)	101 (14.1)	59 (15.4)	198 (26.7)	35 (16.5)	46 (27.0)
Arg/Gly	436 (43.7)	40 (39.6)	78 (46.7)	819 (50.6)	402 (50.8)	330 (45.8)	167 (43.5)	355 (48.0)	87 (41.0)	96 (56.5)
Gly/Gly	408 (40.9)	47 (46.5)	64 (38.3)	493 (30.5)	265 (33.5)	289 (40.1)	158 (41.1)	187 (25.3)	90 (42.5)	28 (16.5)
Subjects with data on rs1042714. n.	998	101	167	1,622	791	722	384	744	212	169
Risk allele (Gln) frequency	0.56	0.60	0.58	0.78	0.63	0.56	0.54	0.82	0.60	0.93
rs1042714 genotype, no. (%)										
Gln/Gln	307 (30.8)	36 (35.6)	57 (34.1)	971 (59.9)	313 (39.6)	232 (32.1)	115 (30.0)	497 (66.8)	81 (38.2)	144 (85.2)
Gln/Glu	495 (49.6)	50 (49.5)	79 (47.3)	576 (35.5)	376 (47.5)	349 (48.4)	184 (47.9)	223 (30.0)	91 (42.9)	25 (14.8)
Glu/Glu	196 (19.6)	15 (14.9)	31 (18.6)	75 (4.6)	102 (12.9)	141 (19.5)	85 (22.1)	24 (3.2)	40 (18.9)	0 (0.0)
Subjects with data on both SNPs. n.	998	101	167	1,618	791	714	384	740	212	169
Haplotype frequency										
Arg16/Gln27	0.37	0.34	0.38	0.44	0.41	0.37	0.37	0.51	0.37	0.55
Gly16/Gln27	0.18	0.27	0.20	0.34	0.22	0.19	0.17	0.31	0.23	0.37
Gly16/Glu27	0.45	0.39	0.42	0.22	0.37	0.44	0.46	0.18	0.40	0.08
Linkage disequilibrium between rs1042713 and rs1042714										
r^2 (D`)	0.47 (~1)	0.33 (1)	0.43 (0.98)	0.23 (1)	0.40 (~1)	0.46 (~1)	0.50 (~1)	0.23 (1)	0.40 (1)	0.10 (1)

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Table 3: Risk of asthma exacerbations* across the other treatment groups.

Haplotypes	BREATHE	ESTATe	follow-MAGICS	GALA II	PACMAN	PAGES	PASS	SAGE	SLOVENIA	SCSGES	Total Combined Results
OR (95% CI) for asthma exacerbations in patients treated with as-required SABA											
	n = 173	**N/A**	**N/A**	**n = 557**	**N/A**	**n = 51**	**N/A**	**n = 192**	**N/A**	**N/A**	**n = 973**
Arg16Gln27 vs. Gly16Glu27	1.28 (0.61, 2.70)	N/A	N/A	1.17 (0.84, 1.62)	N/A	0.54 (0.13, 2.31)	N/A	0.67 (0.36, 1.24)	N/A	N/A	1.00 (0.71, 1.40) $I^2 = 21.50\%$
Arg16Gln27 vs. Gly16Gln27	0.92 (0.33, 2.60)	N/A	N/A	1.13 (0.80, 1.60)	N/A	2.10 (0.26, 17.03)	N/A	0.80 (0.42, 1.55)	N/A	N/A	1.05 (0.79, 1.41) $I^2 = 0.00\%$
Gly16Gln27 vs. Gly16Glu27	1.40 (0.50, 3.97)	N/A	N/A	1.03 (0.73, 1.45)	N/A	0.26 (0.03, 2.09)	N/A	0.83 (0.43, 1.61)	N/A	N/A	0.99 (0.74, 1.32) $I^2 = 0.00\%$
OR (95% CI) for asthma exacerbations in patients treated with ICS monotherapy											
	n = 562	**n = 65**	**N/A**	**n = 527**	**n = 484**	**n = 268**	**n = 29**	**n = 341**	**n = 178**	**n = 169**	**n = 2,623**
Arg16Gln27 vs. Gly16Glu27	1.21 (0.88, 1.65)	0.74 (0.31, 1.76)	N/A	1.47 (1.00, 2.16)	0.74 (0.45, 1.21)	1.21 (0.80, 1.82)	N/A	0.70 (0.45, 1.09)	0.72 (0.44, 1.18)	1.00 (0.38, 2.62)	0.98 (0.78, 1.23) $I^2 = 46.37\%$
Arg16Gln27 vs. Gly16Gln27	1.06 (0.72, 1.56)	1.58 (0.58, 4.30)	N/A	1.22 (0.88, 1.70)	0.96 (0.54, 1.71)	0.99 (0.61, 1.60)	N/A	1.01 (0.99, 1.02)	0.93 (0.50, 1.70)	0.67 (0.39, 1.15)	1.01 (0.99, 1.02) $I^2 = 0.00\%$
Gly16Gln27 vs. Gly16Glu27	1.15 (0.78, 1.70)	0.47 (0.16, 1.37)	N/A	1.74 (1.15, 2.62)	0.77 (0.43, 1.36)	1.25 (0.78, 2.00)	0.67 (0.34, 4.97)	0.70 (0.43, 1.14)	0.78 (0.43, 1.42)	1.49 (0.55, 4.04)	1.01 (0.77, 1.33) $I^2 = 46.05\%$
OR (95% CI) for asthma exacerbations in patients treated with ICS+LTRA											
	n = 37	**N/A**	**N/A**	**n = 203**	**N/A**	**n = 64**	**N/A**	**n = 34**	**N/A**	**N/A**	**n = 338**
Arg16Gln27 vs. Gly16Glu27	0.96 (0.29, 3.24)	N/A	N/A	1.33 (0.72, 2.45)	N/A	1.01 (0.44, 2.27)	N/A	1.11 (0.19, 6.55)	N/A	N/A	1.16 (0.75, 1.80) $I^2 = 0.00\%$
Arg16Gln27 vs. Gly16Gln27	1.14 (0.32, 4.07)	N/A	N/A	0.96 (0.60, 1.52)	N/A	0.43 (0.14, 1.25)	N/A	1.50 (0.41, 5.54)	N/A	N/A	0.91 (0.62, 1.34) $I^2 = 0.00\%$
Gly16Gln27 vs. Gly16Glu27	0.84 (0.25, 2.90)	N/A	N/A	1.39 (0.75, 2.60)	N/A	2.36 (0.72, 7.78)	N/A	0.74 (0.11, 5.04)	N/A	N/A	1.35 (0.83, 2.20) $I^2 = 0.00\%$
OR (95% CI) for asthma exacerbations in patients treated with ICS+LABA+LTRA											
	n = 84	**N/A**	**N/A**	**n = 129**	**n = 43**	**n = 168**	**n = 229**	**n = 33**	**N/A**	**N/A**	**n = 686**
Arg16Gln27 vs. Gly16Glu27	0.81 (0.42, 1.58)	N/A	N/A	0.96 (0.38, 2.44)	0.41 (0.08, 2.14)	0.97 (0.56, 1.68)	1.58 (0.89, 2.83)	0.65 (0.10, 4.31)	N/A	N/A	1.03 (0.75, 1.41) $I^2 = 2.57\%$
Arg16Gln27 vs. Gly16Gln27	1.53 (0.63, 3.72)	N/A	N/A	0.84 (0.40, 1.79)	0.27 (0.04, 1.63)	1.82 (0.93, 3.57)	1.40 (0.65, 3.01)	0.26 (0.02, 3.31)	N/A	N/A	1.22 (0.83, 1.79) $I^2 = 5.91\%$
Gly16Gln27 vs. Gly16Glu27	0.53 (0.21, 1.35)	N/A	N/A	1.13 (0.45, 2.87)	1.52 (0.36, 6.47)	0.53 (0.28, 1.00)	1.13 (0.56, 2.29)	2.48 (0.18, 34.37)	N/A	N/A	0.83 (0.54, 1.26) $I^2 = 17.70\%$

*Asthma exacerbations, asthma–related hospitalizations/emergency department visit or oral corticosteroids use. SABA, short-acting β_2-agonists; ICS, inhaled corticosteroids; LABA, long-acting β_2-agonists; LTRA, leukotriene receptor antagonists. Odds Ratio (ORs) and corresponding 95% Confidence Intervals (CIs) were reported, adjusted for age and sex. N/A, Not applicable.

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FIGURE LEGENDS

Figure1: Forest plots of the association between the *ADRB2* haplotypes and the risk of asthma exacerbations (asthma-related hospitalizations/emergency department visits or oral corticosteroids use) in ICS plus LABA treatment group across studies These plots describe Odds Ratios (ORs) and corresponding 95% Confidence Intervals (CIs), adjusted for age and sex.

Figure 2: Forest plots of the association between the *ADRB2* haplotypes and the risk of asthma-related oral corticosteroids use in ICS plus LABA treatment group across studies. These plots describe Odds Ratios (ORs) and corresponding 95% Confidence Intervals (CIs), adjusted for age and sex.

Figure 3: Forest plots of the association between the *ADRB2* haplotypes and the risk of asthma-related hospitalizations/emergency department visits in ICS plus LABA treatment group across studies. These plots describe Odds Ratios (ORs) and corresponding 95% Confidence Intervals (CIs), adjusted for age and sex.

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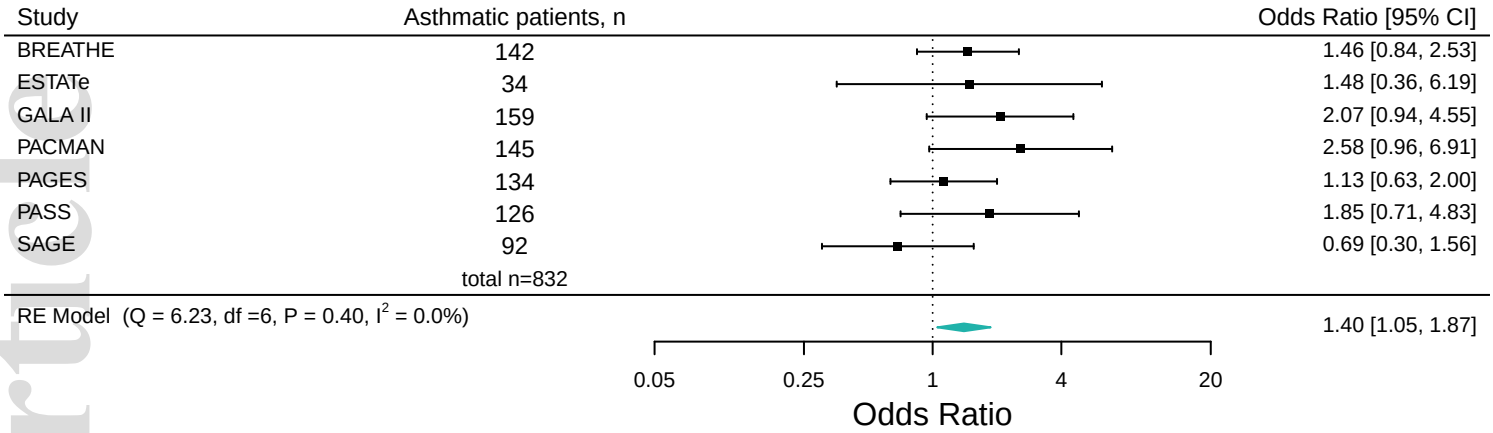
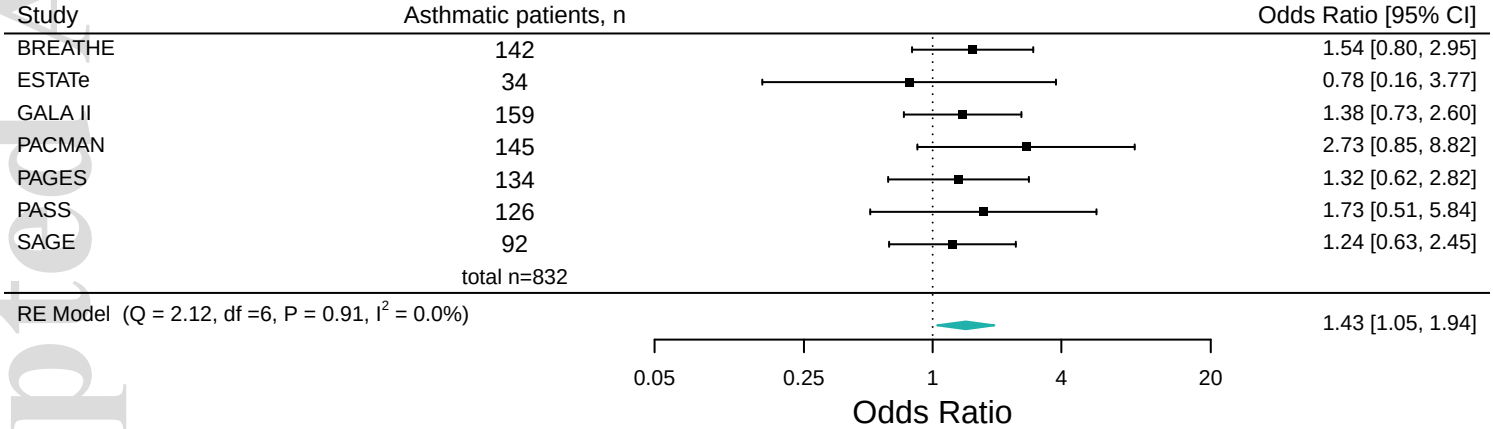
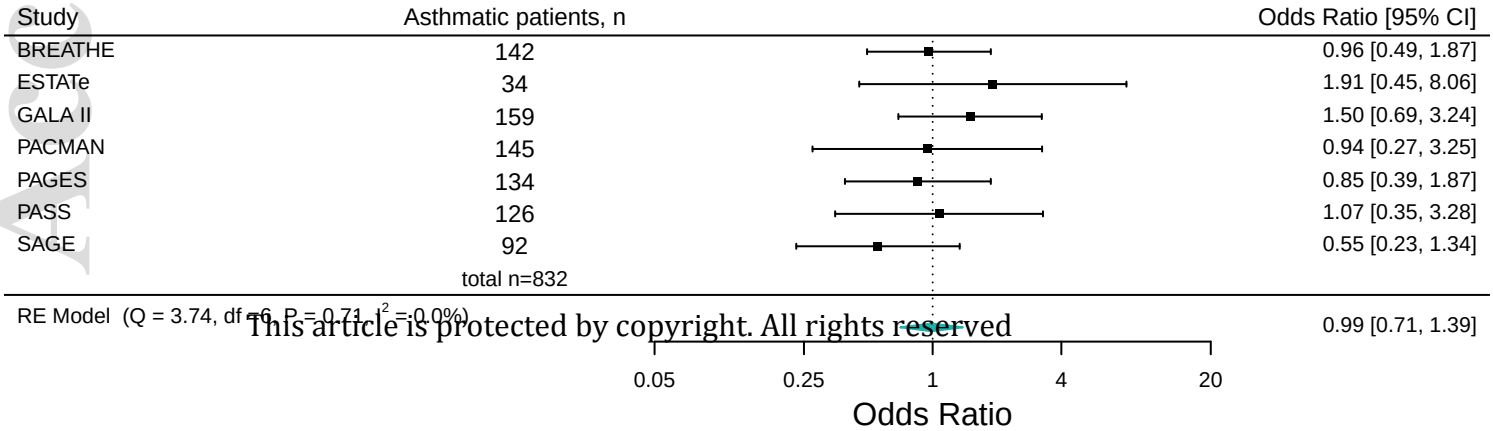
a) Arg16/Gln27 vs. Gly16/Glu27



b) Arg16/Gln27 vs. Gly16/Gln27



c) Gly16/Gln27 vs. Gly16/Glu27



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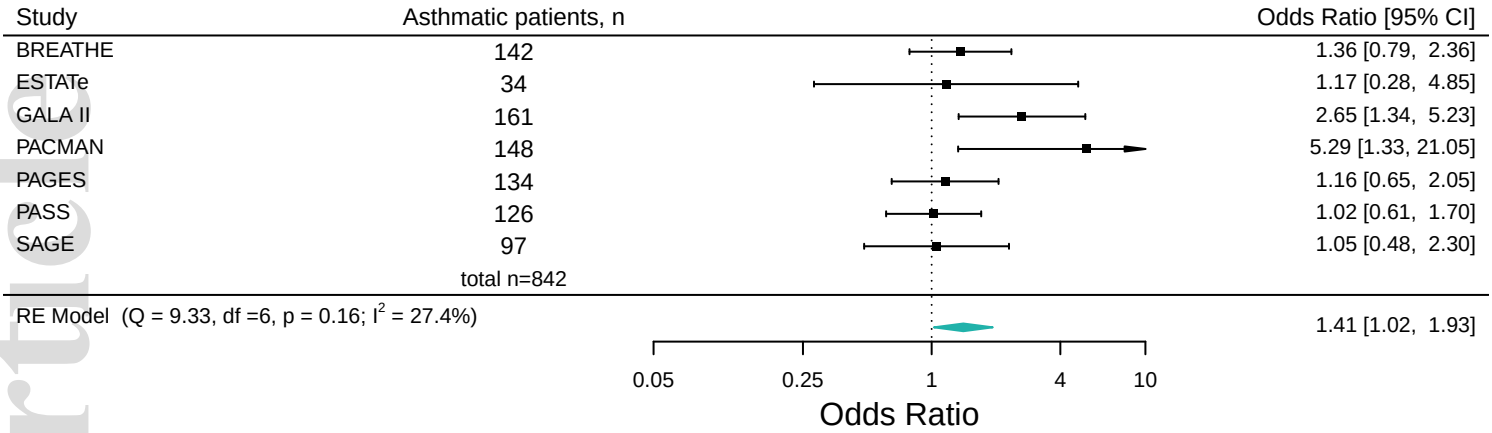
a) Arg16/Gln27 vs. Gly16/Glu27



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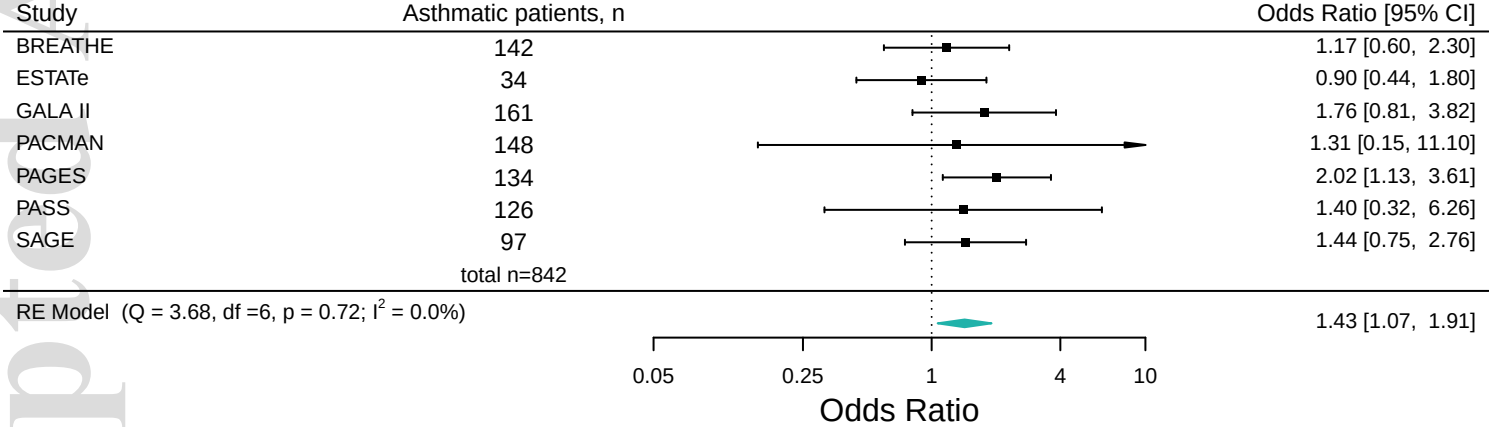
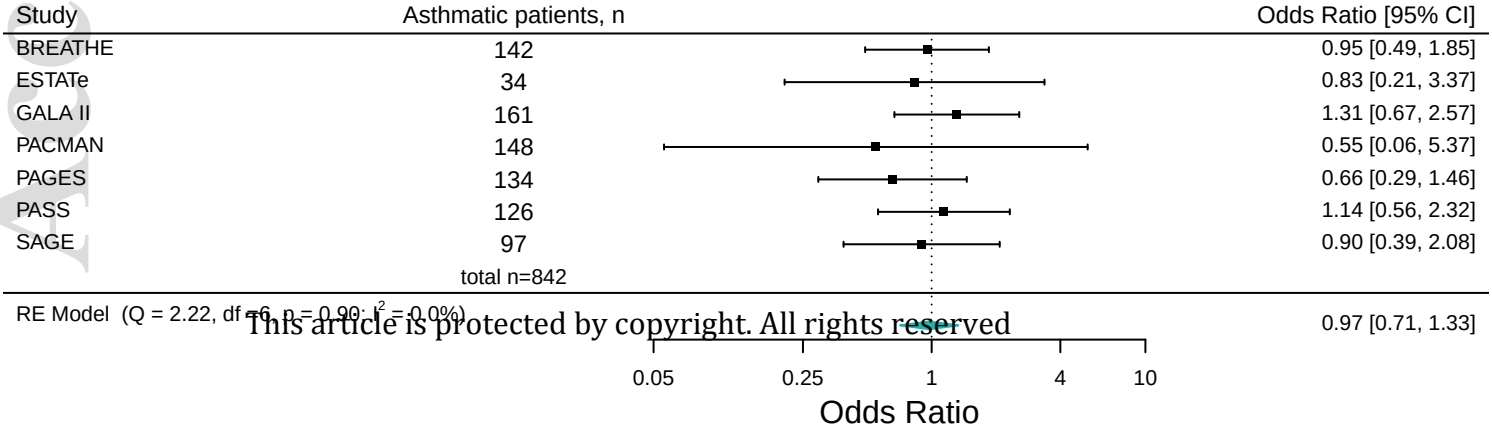


c) Gly16/Gln27 vs. Gly16/Glu27



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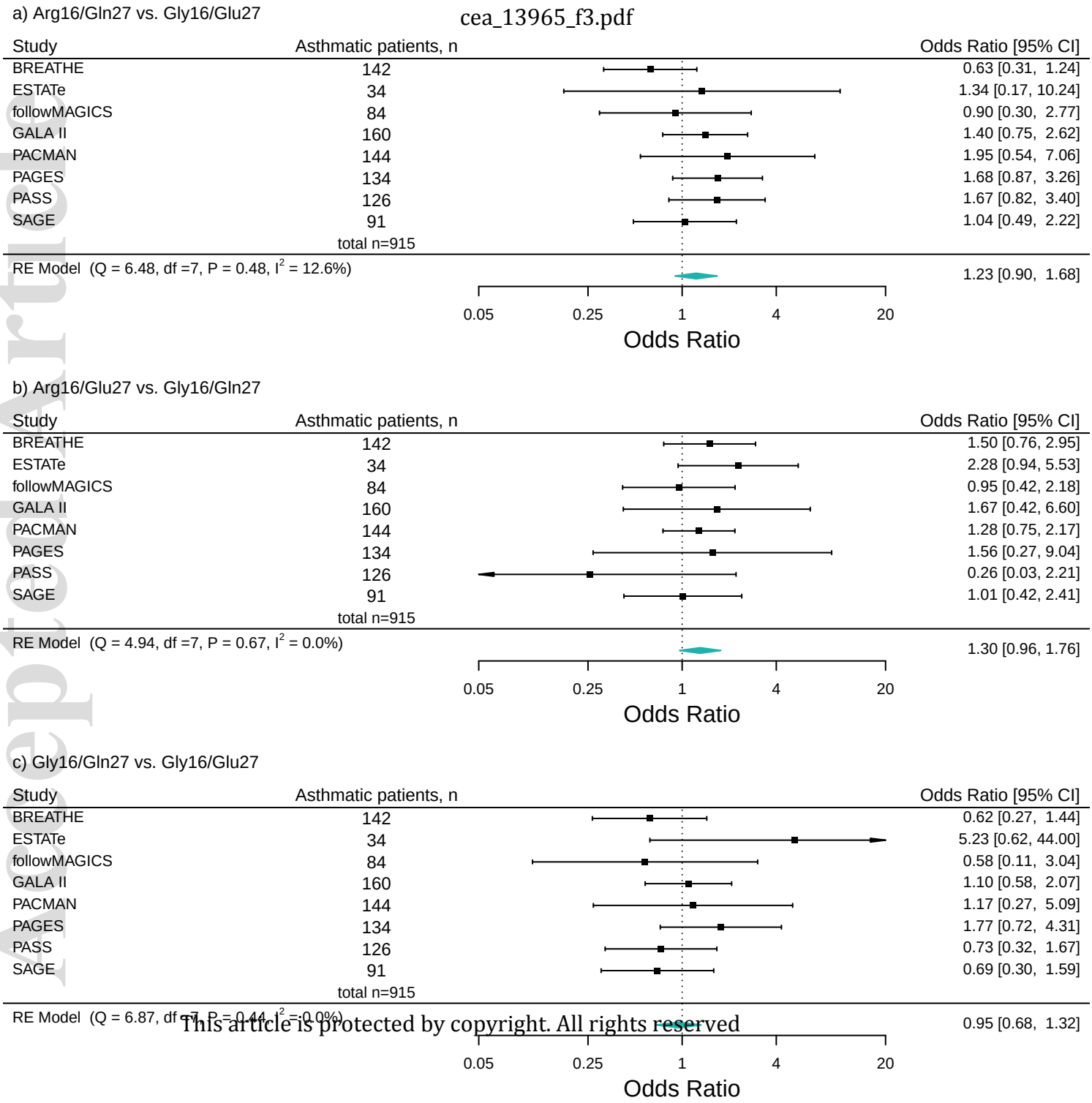

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ADRB2 Haplotypes and Asthma Exacerbations in Children and Young Adults: An Individual Participant Data Meta-Analysis

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Supplemental Methods

Study Population

Data of ten independent studies participating in the Pharmacogenomics in Childhood of Asthma (PiCA) consortium[1] were analyzed. All the studies have been approved by their local medical ethics committees and parents and/or participants provided written consent.

BREATHE is an observational study that includes children and young adults (age: 3-22 years)[2] with physician-diagnosed asthma recruited from primary and secondary care units in Tayside, Scotland, and Brighton, United Kingdom. A detailed history including information on symptoms, treatment, asthma exacerbations, demographics, and anthropometric information was obtained from the participants. From 1,307 individuals, mouthwash samples were collected for DNA analysis and the patients were considered to be non-Hispanic whites.

The Effectiveness and Safety of Treatment with Asthma Therapy in children *(ESTATe)*, www.estate-studie.nl, is a case-control study that includes children and young adults (age: 4-19 years) with physician-diagnosed asthma recruited from primary care units in the Netherlands. Patients were selected from either the IPCI (Interdisciplinary Processing of Clinical Information) database or the PHARMO Database Network. Both databases contain the complete electronic medical records of more than one million patients throughout the Netherlands with detailed information on patient diagnosis, patient prescription (IPCI), or patient dispensing (PHARMO). During the study period (2000-2012), all children with asthma, 4 years or older and treated with asthma controller therapy were selected. Within this cohort, asthma exacerbation cases were defined as the use of systemic corticosteroids, asthma-related emergency department visits, or hospitalization. Each case was matched to four controls on age, sex, general practice (GP), and type of asthma controller therapy. Next, all potential cases and controls were invited to participate via their respective GP. If patients

agreed to participate, they completed a research questionnaire, including questions on asthma control, and provided a saliva sample (for DNA extraction).

The *followMAGICS* study is the follow-up study of the observational Multicenter Asthma Genetics in Childhood Study (MAGICS), which includes physician-diagnosed asthmatic children and young adults (age: 7-25 years)[3] recruited from secondary and tertiary centers in Germany and Austria. The ethnicity of patients was non-Hispanic whites, which was validated through principal component analysis.

The Genes-Environment and Admixture in Latino Americans (*GALA II*) and the Study of African Americans, Asthma, Genes, and Environments (*SAGE)* studies are two independent case-control asthma cohorts that focus on two different racial/ethnic groups based on the self-identified ethnicity of the four grandparents of each subject: Hispanics/Latinos (GALA II) and African Americans (SAGE). Both studies recruited unrelated children and young adults (age: 8- 21 years) using the same protocol and questionnaires from different areas in the United States and Puerto Rico (Chicago, Illinois; New York City, New York; Houston, Texas; San Francisco, California; and San Juan, Puerto Rico) for GALA.SAGE only recruited participants from the San Francisco Bay Area and California.[4,5] Cases were defined as subjects with physician-diagnosed asthma. Exclusion criteria were established as any of the following: ≥10 pack-years of smoking; any smoking within one year of the recruitment date; in the third trimester of pregnancy; or a history of any one of the following: sickle cell disease, cystic fibrosis, sarcoidosis, cerebral palsy, or heart or chest surgery. Exacerbations were defined as a patient-reported occurrence of at least one of the following asthma-related events during the last 12 months preceding study enrolment: emergency care, hospitalization, and oral corticosteroids use.

The Pharmacogenetics of Asthma Medication in Children Medication with Anti-inflammatory effects (*PACMAN*) study in the Netherlands,[6] is an observational cohort study

that included children (age: 4-12 years) old with self-reported regular use of asthma medication recruited through community pharmacies. Children were selected from community pharmacies in the Netherlands that belonged to the Utrecht Pharmacy Practice Network for Education and Research (UPPER).[7] During visits to community pharmacies, detailed information on exacerbations and medication over the last 12 months was collected. Dutch, Moroccan, and Turkish ethnicities were considered Caucasian.

The Pediatric Asthma Gene Environment Study (*PAGES*) was a cross-sectional observational study designed to relate asthma outcomes to environmental end genetic factors. Children with physician-diagnosed asthma were recruited from primary care (age: 5-16 years) and secondary care (ages 2-16 years) centers across Scotland.[8] In a single assessment, participants completed questionnaires with questions on demographic characteristics, asthma control, treatment, quality of life, and diet. Physiological testing was completed in a subgroup of participants and saliva was obtained for DNA extraction.[8]

The Pharmacogenetics of Adrenal Suppression Study (PASS) from the United Kingdom (age: 5-18 years) is a multicenter cohort of asthmatic children. The study initially aimed to explore the association between the use of corticosteroids and adrenal suppression. Children with asthma diagnosed by a secondary care pediatrician requiring inhaled corticosteroid therapy with clinical concern about adrenal suppression were included. The ethnicity of patients was self-reported as non-Hispanic whites.[9,10]

The Singapore Cross Sectional Genetic Epidemiology Study (*SCSGES*) (age: 6-31 years)[11] is an ongoing cross-sectional genetic epidemiology study on allergic diseases among Singapore Chinese individuals. Volunteers were of Chinese ethnicity and resident in Singapore, and their DNA was extracted from mouthwash and blood. The ethnicity of subjects was self-reported Chinese and confirmed by principal component analysis between previous genome-wide genotyping data and Han Chinese (CHB) population from the HapMap project.[11,12]

Asthma was defined as having a physician diagnosis of asthma symptoms prior to recruitment. The *SLOVENIA* study is a case-control cohort (age: 5-18) and includes asthmatic children and young adults recruited from tertiary health centers from Murska Sobota, Slovenia. Asthma was defined by physician diagnosis and hospital records. All patients were self-identified Caucasians of Slovenian origin.[13]

Supplemental Results

Table S1: Functional annotation of rs1042713 using the HaploRegv4.1[14]

Chr	pos (hg38)	LD (r^2)	LD (D')	variant	Ref	Alt	EUR freq	Enhancer histone marks	DNAse	Motifs changed	Selected eQTL hits	GENCODE genes
5	148819704	0.9	0.95	rs35283004	A	G	0.38	BLD, MUS		GR,Maf	2 hits	6.9kb 5' of *ADRB2*
5	148820281	0.81	0.92	rs71582318	T	C	0.37	BLD, SKIN		Pou1f1,TATA		6.3kb 5' of *ADRB2*
5	148821442	0.94	0.97	rs12189018	T	C	0.38	BLD		RXRA	2 hits	5.2kb 5' of *ADRB2*
5	148822166	0.94	0.97	rs35019280	AG	A	0.38	BLD		CIZ,GATA,HNF1	2 hits	4.4kb 5' of *ADRB2*
5	148822926	0.93	0.97	rs33910799	AG	A	0.38	BLD	BD	CEBPB,DMRT2	1 hit	3.7kb 5' of *ADRB2*
5	148825014	0.97	0.99	rs17778257	A	T	0.38	9 tissues	SKIN	5 altered motifs	4 hits	1.6kb 5' of *ADRB2*
5	148826178	0.96	0.98	rs12654778	G	A	0.38		38 tissues	Foxp3,p53	4 hits	414bp 5' of *ADRB2*
5	148826877	1	1	rs1042713	G	A	0.38		28 tissues	4 altered motifs	3 hits	*ADRB2*

Pos; position, LD; Linkage disequilibrium, Ref; reference, Alt; alternative, EUR freq; European frequency, eQTL; expression quantitative trait loci

Table S2: Functional annotation of rs1042714 using the HaploRegv4.1[14]

chr	pos (hg38)	LD (r^2)	LD (D')	variant	Ref	Alt	EUR freq	Enhancer histone marks	DNAse	Motifs changed	Selected eQTL hits	GENCODE genes
5	148819436	0.88	0.94	rs4705059	C	T	0.59	BLD, HRT, MUS	HRT	5 altered motifs		7.2kb 5' of *ADRB2*
5	148819441	0.88	0.94	rs4705060	G	A	0.59	BLD, MUS		4 altered motifs		7.2kb 5' of *ADRB2*
5	148819679	0.9	0.96	rs10078004	G	A	0.60			Mrg,NRSF		6.9kb 5' of *ADRB2*
5	148819882	0.9	0.96	rs67339154	A	G	0.60	BLD		Brachyury,TBX5		6.7kb 5' of *ADRB2*
5	148820448	0.94	0.97	rs56330463	T	C	0.59	BLD, SKIN		PPAR		6.1kb 5' of *ADRB2*
5	148820990	0.94	0.98	rs2082382	G	A	0.60	BLD	38 tissues	Foxo,Rad21	2 hits	5.6kb 5' of *ADRB2*
5	148821037	0.97	0.99	rs2082395	A	G	0.59	BLD	25 tissues	5 altered motifs	2 hits	5.6kb 5' of *ADRB2*
5	148821395	0.95	0.99	rs9325120	C	A	0.58	BLD		4 altered motifs		5.2kb 5' of *ADRB2*
5	148821692	0.97	0.99	rs11168066	C	A	0.59	BLD		Dmbx1,Otx2	2 hits	4.9kb 5' of *ADRB2*
5	148821753	0.96	0.99	rs11959615	T	A	0.59	BLD			2 hits	4.8kb 5' of *ADRB2*
5	148821910	0.97	0.99	rs35875547	AT	A	0.59	BLD, BRN		10 altered motifs		4.7kb 5' of *ADRB2*
5	148821922	0.97	0.99	rs11958940	A	T	0.59	BLD, BRN		NRSF,Zbtb3		4.7kb 5' of *ADRB2*
5	148822006	0.97	0.99	rs34064454	A	G	0.59	BLD, BRN		AIRE,Pax-4		4.6kb 5' of *ADRB2*
5	148823105	0.97	0.99	rs11746634	C	G	0.59	ESC, BLD		LUN-1,RORalpha1		3.5kb 5' of *ADRB2*
5	148823238	0.97	0.99	rs11168067	A	G	0.59	BLD		NRSF,Pitx2,SETDB1		3.4kb 5' of *ADRB2*
5	148823373	0.95	0.99	rs9325122	C	T	0.60	BLD		HDAC2,Pou2f2,Pou3f3		3.2kb 5' of *ADRB2*
5	148824199	0.97	0.99	rs1432622	T	C	0.59	BLD		7 altered motifs	2 hits	2.4kb 5' of *ADRB2*
5	148824445	0.97	0.99	rs1432623	C	T	0.59	BLD, SKIN		Nkx2		2.1kb 5' of *ADRB2*
5	148824558	0.97	0.99	rs11168068	C	T	0.59	BLD, SKIN		8 altered motifs		2kb 5' of *ADRB2*
5	148825489	0.97	0.99	rs2400707	A	G	0.59	12 tissues	SKIN,SKIN	HLF	2 hits	1.1kb 5' of *ADRB2*
5	148825809	0.97	0.99	rs2053044	A	G	0.59	5 tissues	35 tissues	8 altered motifs		783bp 5' of *ADRB2*
5	148826364	0.99	0.99	rs11168070	G	C	0.59		51 tissues	GR		228bp 5' of *ADRB2*
5	148826465	0.99	1	rs11959427	C	T	0.59	BRN	52 tissues	11 altered motifs		127bp 5' of *ADRB2*
5	148826785	0.98	1	rs1042711	C	T	0.59		35 tissues	6 altered motifs		5'-UTR of *ADRB2*
5	148826812	0.98	1	rs1801704	C	T	0.59	BRN	37 tissues	E2A,Sin3Ak-20,ZEB1		5'-UTR of *ADRB2*
5	148826910	1	1	rs1042714	G	C	0.59		21 tissues	GATA,PU.1		*ADRB2*

Pos; position, LD; Linkage disequilibrium, Ref; reference, Alt; alternative, EUR freq; European frequency, eQTL; expression quantitative trait loci

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